Next-Generation Sequencing Sample Submission Guidelines

Sequencing request procedure:

For pricing, invoicing and general sequencing information please contact: genomics@canceratl.ca

We are able to work with our clients from project conception up to bioinformatics analysis to ensure that our clients get the best value for their projects. The Atlantic Cancer Research Institute (ACRI) and the New Brunswick Center for Precision Medicine (NBPCM) will work with you to find the best pricing option for your project(s).

For technical sequencing inquiries and support please contact simic@canceratl.ca.

Sample shipping instructions:

Samples should be shipped on dry ice using FedEx, Purolator or UPS delivery services. Samples should be packaged with enough dry ice to last two-three days of shipping time. We recommend shipping the samples on a Monday to avoid long weekend closures.

Shipping address:

Attn: NGS Sequencing Core
Atlantic Cancer Research Institute
35 Providence Street, 4th Floor,
Moncton, NB, Canada
E1C 8X3
Phone no: 506 862 7576

Sample submission guidelines

DNA sample guidelines:

When submitting nucleic acids for next-generation sequencing technologies, it is recommended to submit samples of the highest possible quality and purity:

- OD 260/280 ratio of 1.8 to 2.0
- OD 260/230 ratio of at least 2.0
- Resuspend DNA samples in 10mM Tris-HCl pH 8.0 with 0.1mM of EDTA
- Quantify samples using fluorometric-based methods to avoid overestimating sample concentrations, resulting in an inadequate amount of starting material
- We offer sample QC using tape station and fragment analyzer and it is recommended to send a separate PCR strip with 5ul of DNA for QC

- For exome sequencing a minimum of 20 samples are required for fast turnaround time due to the high throughput requirement of Novaseq flow cells. Clients can also choose flow cell sharing option if similar library types are available for sequencing at the time (turnaround time might be extended by three weeks or more).

Sample input recommendations:

Library Type	Recommended quantity	Volume	Preferred Buffer
Whole genome-Truseq PCR free	1ug-2 ug	≥100ul	Low TE buffer
Whole genome low input-Collibri (PCR free option available as well)	50ng-500ng	≥50ul	
WG Methyl seq-NEB EM seq	10ng-500 ng	≥50ul	
Whole Exome enrichment Twist/Collibri	50ng-500ng	≥50ul	EDTA free buffer for ES shearing
*Illumina DNA PCR free-Tagmentation	25-300ng	≥50ul	Low TE
Oncomine-Liquid Biopsy panels- Ion Torrent	20ng-50ng	≥50ul	
Oncomine FFPE panels-Ion Torrent	50ng-1ug	≥50ul	

*Will be available soon

RNA sample guidelines:

- Colum based RNA extraction kits preferred
- Quality of the RNA is assessed based on the RIN number. Samples for transcriptome sequencing should have a RIN greater than or equal to 8.
- Re-suspend the samples in nuclease free water
- Integrity of the samples can be assessed at ACRI. We recommended sending a separate PCR strip with 3ul of RNA for QC.

Library type	Recommended quantity	Volume	Preferred Buffer
Stranded RNA-library (poly-A/rRNA)-NEB	10ng-1ug total RNA	≥ 50 ul	Mol.Bio.Grade Water
Non-stranded RNA-library (poly-A/rRNA-NEB	10ng-1ug total RNA	≥50ul	
Quantseq-3'UTR sequencing	10ng-500ng total RNA	≥50 ul	
*Illumina stranded-Total RNA seq	1ng-1ug total RNA	≥50 ul	
Illumina stranded mRNA	25ng-1ug total RNA	≥50 ul	
SmallRNA/microRNA library (from total RNA)-Illumina	2.5ug-500ng	≥ 50 ul	
Exosome/low quality smallRNA/microRNA-TriLink	≥10ng of enriched sRNA; 1-5ug for total RNA	≥10ul	
RNA-seq library (poly-A& rRNA depleted)-Ion Torrent	20ug total RNA (min 10ug)	≥100ul	
SmallRNA/microRNA-Ion Torrent	≥5ug (min 1ug)	≥100ul	

*Will be available soon